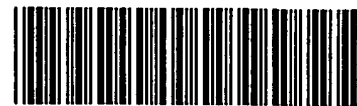


## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/594,707  
Source: FWP  
Date Processed by STIC: 10/6/06

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IFWP

## RAW SEQUENCE LISTING

DATE: 10/06/2006

PATENT APPLICATION: US/10/594,707

TIME: 11:17:33

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\10062006\J594707.raw

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3 <110> APPLICANT: OHARA, Osamu
4     NAGASE, Takahiro
5     OISHI, Michio
6     YOKOTA, Hiroshi
7     KAMIDA, Osamu
9 <120> TITLE OF INVENTION: Gene encoding a guanine nucleotide exchange factor and the
gene product
10     thereof
12 <130> FILE REFERENCE: 3190-100
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/594,707
15 <141> CURRENT FILING DATE: 2006-09-28
17 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/005918
18 <151> PRIOR FILING DATE: 2005-03-31
20 <150> PRIOR APPLICATION NUMBER: JP P2004-106268
21 <151> PRIOR FILING DATE: 2004-03-31
23 <160> NUMBER OF SEQ ID NOS: 27
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 4977
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: misc_feature
34 <223> OTHER INFORMATION: Polynucleotide encoding the protein (SEQ ID NO:2) that have a
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35     ction of guanine nucleotide exchange factor.
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (314)..(4336)
43 <220> FEATURE:
44 <221> NAME/KEY: misc_feature
45 <222> LOCATION: (602)..(1126)
46 <223> OTHER INFORMATION: A region encoding Dbl homology domain
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51 <222> LOCATION: (1202)..(1495)
52 <223> OTHER INFORMATION: A region encoding Pleckstrin homology domain
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60 tccggggccag ctgagggggt ggcgggtgggc gggagcggtc ggcggcctca gccccttcag      180
62 agagcgactt tcaaactcgc gccgcgctcg cggcagcacc tgggcagccc cgcacgccgt      240
64 gcgcgtcccc agcccgcggg gcagctaccg ctcgaaatctc cctgggggtgc cctccccagg      300
66 cagcaatgcc agg atg cct gtg tcc acc tcc ctc cac cag gat ggc agc      349

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67

Met Pro Val Ser Thr Ser Leu His Gln Asp Gly Ser

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74	tcc	tgt	gac	agt	cgc	agt	gcc atg gag gag ccc agc agc tcc gag gct	445
75	Ser	Cys	Asp	Ser	Arg	Ser	Ala Met Glu Glu Pro Ser Ser Ser Glu Ala	
76		30				35		40
78	ccc	gcc	aag	aat	ggg	gca	ggc tcc ctg aga agc cgg cat ctg ccc aac	493
79	Pro	Ala	Lys	Asn	Gly	Ala	Gly Ser Leu Arg Ser Arg His Leu Pro Asn	
80	45				50			55
82	agc	aac	aac	aac	tcc	agc	agc tgg ttg aac gtg aag ggg ccc ctc tcc	541
83	Ser	Asn	Asn	Asn	Ser	Ser	Ser Trp Leu Asn Val Lys Gly Pro Leu Ser	
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86	ccg	ttc	aac	agc	cgg	gca	gcg gca ggg cct gca cac cac aag ctc agc	589
87	Pro	Phe	Asn	Ser	Arg	Ala	Ala Ala Gly Pro Ala His His Lys Leu Ser	
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90	tac	ctg	ggc	cga	gtg	gtg	cgg gag atc gtg gag aca gag cgc atg tac	637
91	Tyr	Leu	Gly	Arg	Val	Val	Arg Glu Ile Val Glu Thr Glu Arg Met Tyr	
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94	gta	cag	gac	ctg	cgc	agc	atc gtg gag gac tac ctc ttg aag atc att	685
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98	gac	aca	ccc	ggg	ctg	ctg	aag cca gaa cag gtc agc gcc ctc ttt ggg	733
99	Asp	Thr	Pro	Gly	Leu	Leu	Lys Pro Glu Gln Val Ser Ala Leu Phe Gly	
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102	aac	ata	gaa	aac	atc	tac	gcg ctg aac agc cag ctc ctc aga gac ctg	781
103	Asn	Ile	Glu	Asn	Ile	Tyr	Ala Leu Asn Ser Gln Leu Leu Arg Asp Leu	
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106	gac	agc	tgc	aat	agt	gac	ccc gtg gct gtg gcc agc tgc ttt gtg gaa	829
107	Asp	Ser	Cys	Asn	Ser	Asp	Pro Val Ala Val Ala Ser Cys Phe Val Glu	
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110	agg	agc	caa	gag	ttt	gat	atc tac act cag tat tgc aac aat tac ccc	877
111	Arg	Ser	Gln	Glu	Phe	Asp	Ile Tyr Thr Gln Tyr Cys Asn Asn Tyr Pro	
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115	Asn	Ser	Val	Ala	Ala	Leu	Thr Glu Cys Met Arg Asp Lys Gln Gln Ala	
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118	aag	ttc	ttt	cgg	gac	cgg	cag gag ctg cta cag cac tcg ctg ccc ttg	973
119	Lys	Phe	Phe	Arg	Asp	Arg	Gln Glu Leu Leu Gln His Ser Leu Pro Leu	
120	205				210			215
122	ggc	tcc	tac	ctg	ctg	aag	cca gtc cag cgc atc ctc aag tac cac ctg	1021
123	Gly	Ser	Tyr	Leu	Leu	Lys	Pro Val Gln Arg Ile Leu Lys Tyr His Leu	
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126	ctg	ctc	cag	gaa	att	gcc	aaa cat ttt gat gaa gaa gag gat ggc ttt	1069
127	Leu	Leu	Gln	Glu	Ile	Ala	Lys His Phe Asp Glu Glu Glu Asp Gly Phe	
128					240			245
130	gag	gtg	gtg	gag	gat	gcc	att gac acc atg acc tgt gtg gcc tgg tac	1117
131	Glu	Val	Val	Glu	Asp	Ala	Ile Asp Thr Met Thr Cys Val Ala Trp Tyr	
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136		270					275					280					
138	att	cag	tca	ctc	ctc	atc	aac	tgg	aag	ggg	ccc	gac	ctg	acc	acc	tac	1213
139	Ile	Gln	Ser	Leu	Leu	Ile	Asn	Trp	Lys	Gly	Pro	Asp	Leu	Thr	Thr	Tyr	
140	285					290					295					300	
142	ggg	gag	ctt	gtc	ctg	gag	ggc	aca	ttc	cgc	gtg	cat	cgc	gtg	cgc	aat	1261
143	Gly	Glu	Leu	Val	Leu	Glu	Gly	Thr	Phe	Arg	Val	His	Arg	Val	Arg	Asn	
144				305						310					315		
146	gaa	agg	acc	ttt	ttc	ctc	ttt	gac	aaa	aca	ctg	ctt	atc	acc	aag	aag	1309
147	Glu	Arg	Thr	Phe	Phe	Leu	Phe	Asp	Lys	Thr	Leu	Leu	Ile	Thr	Lys	Lys	
148				320					325						330		
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151	Arg	Gly	Asp	His	Phe	Val	Tyr	Lys	Gly	Asn	Ile	Pro	Cys	Ser	Ser	Leu	
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154	atg	ctg	atc	gaa	agc	acc	aga	gac	tcc	ctg	tgc	ttc	act	gtc	acc	cac	1405
155	Met	Leu	Ile	Glu	Ser	Thr	Arg	Asp	Ser	Leu	Cys	Phe	Thr	Val	Thr	His	
156		350						355				360					
158	tac	aag	cac	agc	aag	cag	cag	tac	agc	atc	cag	gcc	aag	aca	gtg	gag	1453
159	Tyr	Lys	His	Ser	Lys	Gln	Gln	Tyr	Ser	Ile	Gln	Ala	Lys	Thr	Val	Glu	
160	365					370					375					380	
162	gag	aaa	cgg	aac	tgg	act	cac	cac	atc	aag	agg	ctc	atc	cta	gag	aac	1501
163	Glu	Lys	Arg	Asn	Trp	Thr	His	His	Ile	Lys	Arg	Leu	Ile	Leu	Glu	Asn	
164				385						390					395		
166	cac	cat	gcc	acc	att	ccc	cag	aag	gcc	aag	gaa	gcc	atc	ttg	gaa	atg	1549
167	His	His	Ala	Thr	Ile	Pro	Gln	Lys	Ala	Lys	Glu	Ala	Ile	Leu	Glu	Met	
168				400						405					410		
170	gat	tcc	tat	tat	ccc	aat	cgg	tac	cgc	tgc	agc	cca	gag	cgg	ctg	aag	1597
171	Asp	Ser	Tyr	Tyr	Pro	Asn	Arg	Tyr	Arg	Cys	Ser	Pro	Glu	Arg	Leu	Lys	
172			415					420						425			
174	aag	gct	tgg	tcc	tcc	cag	gat	gag	gtg	tcc	acc	aat	gtg	cgc	cag	ggg	1645
175	Lys	Ala	Trp	Ser	Ser	Gln	Asp	Glu	Val	Ser	Thr	Asn	Val	Arg	Gln	Gly	
176		430					435					440					
178	cgc	cgg	caa	tct	gag	cca	acc	aaa	cac	ctg	ctc	agg	caa	ctc	aac	gag	1693
179	Arg	Arg	Gln	Ser	Glu	Pro	Thr	Lys	His	Leu	Arg	Gln	Leu	Asn	Glu		
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183	Lys	Ala	Arg	Ala	Ala	Gly	Met	Lys	His	Ala	Gly	Ser	Ala	Gly	Thr	Leu	
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186	ctg	gac	ttt	ggg	cag	ccc	tcc	cgt	act	cgg	ggc	ctg	cag	cca	gag	gct	1789
187	Leu	Asp	Phe	Gly	Gln	Pro	Ser	Arg	Thr	Arg	Gly	Leu	Gln	Pro	Glu	Ala	
188				480						485					490		
190	gaa	ggg	gct	acc	cag	gag	gag	gaa	gag	gaa	gag	gag	gag	gtg	gtg	gag	1837
191	Glu	Gly	Ala	Thr	Gln	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Val	Val	Glu	
192			495					500						505			
194	gag	gag	gag	gag	gag	gag	gag	gaa	gag	cag	gcc	ttt	cag	gtc	tct	ctg	1885
195	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gln	Ala	Phe	Gln	Val	Ser	Leu	
196		510						515						520			
198	gag	gac	ctg	aca	ggg	cat	gaa	ggc	aac	gag	aag	ggg	gct	ggg	ccg	gag	1933

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203	Pro	Pro	Gly	Ser	Glu	Glu	Glu	Glu	Glu	Glu	Gln	Glu	Glu	Ser	Leu	Ala	
204					545					550					555		
206	gtg	gcg	gag	cag	gta	gcc	gac	ttt	gcc	agc	tcc	ctg	ctg	gcc	gcc	ctc	2029
207	Val	Ala	Glu	Gln	Val	Ala	Asp	Phe	Ala	Ser	Ser	Leu	Leu	Ala	Ala	Leu	
208					560				565					570			
210	cac	tgc	tgg	cac	tat	cgg	gcc	aac	gct	tta	ctt	ttc	tcc	cgg	ggc	gct	2077
211	His	Cys	Trp	His	Tyr	Arg	Ala	Asn	Ala	Leu	Leu	Phe	Ser	Arg	Gly	Ala	
212					575				580					585			
214	atg	gga	aag	ggg	cgc	agg	gag	tct	gaa	agc	tcc	agg	agc	agc	aga	agg	2125
215	Met	Gly	Lys	Gly	Arg	Arg	Glu	Ser	Glu	Ser	Ser	Arg	Ser	Ser	Arg	Arg	
216		590					595					600					
218	ccc	agt	ggc	cgg	tct	cca	acc	agt	act	gag	aag	cgc	atg	agc	ttc	gag	2173
219	Pro	Ser	Gly	Arg	Ser	Pro	Thr	Ser	Thr	Glu	Lys	Arg	Met	Ser	Phe	Glu	
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222	tcc	att	tct	tcc	ctg	cca	gag	gtt	gag	ccg	gac	cct	gag	gct	ggg	agt	2221
223	Ser	Ile	Ser	Ser	Leu	Pro	Glu	Val	Glu	Pro	Asp	Pro	Glu	Ala	Gly	Ser	
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226	gag	caa	gag	gta	ttt	tct	gct	gtg	gaa	ggg	ccc	agt	gcc	gag	gag	acg	2269
227	Glu	Gln	Glu	Val	Phe	Ser	Ala	Val	Glu	Gly	Pro	Ser	Ala	Glu	Glu	Thr	
228					640					645				650			
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231	Pro	Ser	Asp	Thr	Glu	Ser	Pro	Glu	Val	Leu	Glu	Thr	Gln	Leu	Asp	Ala	
232					655					660				665			
234	cac	cag	ggc	ctt	ctg	ggg	atg	gac	ccc	cca	ggt	gac	atg	gtg	gac	ttc	2365
235	His	Gln	Gly	Leu	Leu	Gly	Met	Asp	Pro	Pro	Gly	Asp	Met	Val	Asp	Phe	
236		670					675					680					
238	gtg	gca	gct	gag	agc	act	gag	gac	ctt	aag	gcc	ctg	agc	agc	gag	gag	2413
239	Val	Ala	Ala	Glu	Ser	Thr	Glu	Asp	Leu	Lys	Ala	Leu	Ser	Ser	Glu	Glu	
240	685					690					695					700	
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243	Glu	Glu	Glu	Met	Gly	Gly	Ala	Ala	Gln	Glu	Pro	Glu	Ser	Leu	Leu	Pro	
244					705					710					715		
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247	Pro	Ser	Val	Leu	Asp	Gln	Ala	Ser	Val	Ile	Ala	Glu	Arg	Phe	Val	Ser	
248					720					725				730			
250	agc	ttc	tct	cgg	cgg	agc	agc	gtg	gca	cag	gag	gac	agc	aag	tcc	agt	2557
251	Ser	Phe	Ser	Arg	Arg	Ser	Ser	Val	Ala	Gln	Glu	Asp	Ser	Lys	Ser	Ser	
252					735					740				745			
254	ggc	ttt	ggg	agc	ccg	cgg	ctg	gtc	agc	cgg	agc	agc	agc	gtg	ctc	agc	2605
255	Gly	Phe	Gly	Ser	Pro	Arg	Leu	Val	Ser	Arg	Ser	Ser	Ser	Val	Leu	Ser	
256		750					755					760					
258	ctg	gag	ggc	agc	gag	aag	ggc	ctg	gcc	cgg	cat	ggc	agt	gcc	aca	gac	2653
259	Leu	Glu	Gly	Ser	Glu	Lys	Gly	Leu	Ala	Arg	His	Gly	Ser	Ala	Thr	Asp	
260	765					770					775				780		
262	tcc	ctc	agc	tgt	cag	ctc	tcc	cca	gaa	gtg	gac	atc	agt	gtg	ggg	gtg	2701
263	Ser	Leu	Ser	Cys	Gln	Leu	Ser	Pro	Glu	Val	Asp	Ile	Ser	Val	Gly	Val	

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268				800				805
270	ggc	tgc	cca	gtg	gag	cct	gac	cgg
271	Gly	Cys	Pro	Val	Glu	Pro	Asp	Arg
272				815				820
274	gca	ctc	tcc	acc	cga	gac	cgg	ctg
275	Ala	Leu	Ser	Thr	Arg	Asp	Arg	Leu
276				830				835
278	tat	gaa	aat	gca	gaa	cac	cat	gat
279	Tyr	Glu	Asn	Ala	Glu	His	His	Asp
280	845							850
282	gag	agc	ctc	tcc	tac	atc	ccc	aaa
283	Glu	Ser	Leu	Ser	Tyr	Ile	Pro	Lys
284								865
286	agg	ttc	aac	agc	ctt	ccc	cgg	cca
287	Arg	Phe	Asn	Ser	Leu	Pro	Arg	Pro
288								885
290	ggg	agc	aag	aga	cag	gtg	ggc	tcc
291	Gly	Ser	Lys	Arg	Gln	Val	Gly	Ser
292								895
294	gag	ctc	cca	gga	cca	agc	cag	gca
295	Glu	Leu	Pro	Gly	Pro	Ser	Gln	Ala
296								910
298	tca	gat	gct	gag	ttc	cgc	cca	tct
299	Ser	Asp	Ala	Glu	Phe	Arg	Pro	Ser
300	925							930
302	gga	atg	gag	tct	tcc	gga	ggg	agc
303	Gly	Met	Glu	Ser	Ser	Gly	Gly	Ser
304								945
306	cag	gcc	aat	ggc	ttt	gac	ctg	cat
307	Gln	Ala	Asn	Gly	Phe	Asp	Leu	His
308								960
310	cat	gag	ctg	gga	gcc	atc	aca	gag
311	His	Glu	Leu	Gly	Ala	Ile	Thr	Glu
312								975
314	agc	tcc	tct	ccc	act	gag	ggg	cgc
315	Ser	Ser	Ser	Pro	Thr	Glu	Gly	Arg
316								990
318	ctg	aaa	gag	ctg	gtg	aag	gag	ctg
319	Leu	Lys	Glu	Leu	Val	Lys	Glu	Leu
320	1005							1010
322	ctg	gtg	gcc	cca	ctg	cac	ccc	cgc
323	Leu	Val	Ala	Pro	Leu	His	Pro	Arg
324	1020							1025
326	atg	gac	agc	cac	gtg	agc	gag	cgc
327	Met	Asp	Ser	His	Val	Ser	Glu	Arg
328	1035							1040
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RAW SEQUENCE LISTING ERROR SUMMARY  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12,13,14,15,16,17,18,19



VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number

L:1006 M:259 W: Allowed number of lines exceeded, <223> Other Information:

L:1007 M:259 W: Allowed number of lines exceeded, <223> Other Information: